

Output 3.2

Genomic markers for octopus and red shrimp

ConFish

- Connectivity among Mediterranean fishery stakeholders and scientists resolves connectivity of fishery populations –

WP3 – STUDYING

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OCTOBER 2018

Using the genotyping by sequencing (GBS) method described in Deliverable 3.5.1, a large number of genomic markers was identified for common octopus (*Octopus vulgaris*) and red shrimp (*Aristeus antennatus*) in the Mediterranean. A total of 79134 and 35552 single nucleotide polymorphisms (SNPs) were found for octopus and shrimp populations respectively. These markers are listed and detailed in the provided annexes (Annex 1 – Genomic markers for octopus and Annex 2 – Genomic markers for shrimp), which form an integral part of this output.

The collected data represents a high-resolution perspective into genomic diversity of common octopus and red shrimp across their range. Considering the geographical distribution of these two species in the Mediterranean, we estimate the area to which these genomic markers can be applied to be at least 87500 km². This area was approximated by: removing the background, land masses and other unwanted sea surfaces from species distribution maps obtained from FAO Aquatic Species Distribution Map Viewer (Figures 1 and 2; <http://www.fao.org/figis/geoserver/factsheets/species.html?species=OCC-m&prj=4326>); investigating the different colour ratios on the obtained image using Image Color Extract tool (http://www.coolphptools.com/color_extract); and applying the obtained values as the percentage of total Mediterranean surface area (approx. 2.5 million km²).



Figure 1 Distribution of *Octopus vulgaris* (in red) in the Mediterranean Sea



Figure 2 Distribution of *Aristeus antennatus* (in red) in the Mediterranean Sea